INPUT SET: S35611.raw

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

```
1                              SEQUENCE LISTING
2
3    (1)    General Information:
4
5       (i) APPLICANT: Dalla-Favera, Riccardo
6
7      (ii) TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
8               MULTIPLE MYELOMA
9
10    (iii) NUMBER OF SEQUENCES: 17
11
12     (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Cooper & Dunham LLP
14           (B) STREET: 1185 Avenue of the Americas
15           (C) CITY: New York
16           (D) STATE: New York
17           (E) COUNTRY: U.S.A.
18           (F) ZIP: 10036
19
20      (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26     (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER:
28           (B) FILING DATE: 1-JUNE-2000
29           (C) CLASSIFICATION:
30
31   (viii) ATTORNEY/AGENT INFORMATION:
32           (A) NAME: White, John P.
33           (B) REGISTRATION NUMBER: 28,678
34           (C) REFERENCE/DOCKET NUMBER: 50995-B
35
36     (ix) TELECOMMUNICATION INFORMATION:
37           (A) TELEPHONE: (212) 278-0400
38           (B) TELEFAX: (212) 391-0525
39
40
41   (2) INFORMATION FOR SEQ ID NO:1:
42
43      (i) SEQUENCE CHARACTERISTICS:
44           (A) LENGTH: 108 amino acids
45           (B) TYPE: amino acid
46           (C) STRANDEDNESS: single
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47                  (D)  TOPOLOGY: linear
48
49          (ii)  MOLECULE TYPE: peptide
50
51
52
53
54          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:
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56          Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
57          1                   5                   10                  15
58
59          Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Ile Phe Arg Ile Pro Trp
60                          20                  25                  30
61
62          Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
63                      35                  40                  45
64
65          Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
66              50                  55                  60
67
68          Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
69          65                  70                  75                  80
70
71          Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
72                          85                  90                  95
73
74          Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
75                          100                 105
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77  (2)  INFORMATION FOR SEQ ID NO:2:
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79          (i)  SEQUENCE CHARACTERISTICS:
80                  (A)  LENGTH: 108 amino acids
81                  (B)  TYPE: amino acid
82                  (C)  STRANDEDNESS: single
83                  (D)  TOPOLOGY: linear
84
85          (ii)  MOLECULE TYPE: peptide
86
87
88
89
90          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:2:
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92          Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
93          1                   5                   10                  15
94
95          Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Val Phe Arg Ile Pro Trp
96                          20                  25                  30
97
98          Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
99                      35                  40                  45
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INPUT SET: S35611.raw

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100
101        Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
102            50                  55                  60
103
104        Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
105        65                  70                  75                  80
106
107        Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
108                        85                  90                  95
109
110        Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
111                    100                  105
112
113    (2) INFORMATION FOR SEQ ID NO:3:
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115        (i) SEQUENCE CHARACTERISTICS:
116            (A) LENGTH: 108 amino acids
117            (B) TYPE: amino acid
118            (C) STRANDEDNESS: single
119            (D) TOPOLOGY: linear
120
121    (ii) MOLECULE TYPE: peptide
122
123
124
125
126    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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128        Arg Met Arg Pro Trp Leu Glu Met Gln Ile Asn Ser Asn Gln Ile Pro
129        1               5                  10                  15
130
131        Gly Leu Ile Trp Ile Asn Lys Glu Glu Met Ile Phe Gln Ile Pro Trp
132                    20                  25                  30
133
134        Lys His Ala Ala Lys His Gly Trp Asp Ile Asn Lys Asp Ala Cys Leu
135            35                  40                  45
136
137        Phe Arg Ser Trp Ala Ile His Thr Gly Arg Tyr Lys Ala Gly Glu Lys
138            50                  55                  60
139
140        Glu Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
141        65                  70                  75                  80
142
143        Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Gln Lys Arg Asn Lys Gly
144                        85                  90                  95
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146        Ser Ser Ala Val Arg Val Tyr Arg Met Leu Pro Pro
147                    100                  105
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149    (2) INFORMATION FOR SEQ ID NO:4:
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151        (i) SEQUENCE CHARACTERISTICS:
152            (A) LENGTH: 108 amino acids
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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/585,023*

DATE: 06/15/2000
TIME: 06:39:58

INPUT SET: S35611.raw

153   (B) TYPE: amino acid
154   (C) STRANDEDNESS: single
155   (D) TOPOLOGY: linear
156
157   (ii) MOLECULE TYPE: peptide
158
159
160
161
162   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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164   Arg Met Arg Pro Trp Leu Glu Glu Gln Ile Asn Ser Asn Thr Ile Pro
165   1   5   10   15
166
167   Gly Leu Lys Trp Leu Asn Lys Glu Lys Lys Ile Phe Gln Ile Pro Trp
168   20   25   30
169
170   Met His Ala Ala Arg His Gly Trp Asp Val Glu Lys Asp Ala Pro Leu
171   35   40   45
172
173   Phe Arg Asn Trp Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp
174   50   55   60
175
176   Lys Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
177   65   70   75   80
178
179   Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys Lys Gly
180   85   90   95
181
182   Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu
183   100   105
184
185   (2) INFORMATION FOR SEQ ID NO:5:
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187   (i) SEQUENCE CHARACTERISTICS:
188   (A) LENGTH: 107 amino acids
189   (B) TYPE: amino acid
190   (C) STRANDEDNESS: single
191   (D) TOPOLOGY: linear
192
193   (ii) MOLECULE TYPE: peptide
194
195
196
197
198   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
199
200   Arg Leu Arg Gln Trp Leu Ile Glu Gln Ile Asp Ser Ser Met Tyr Pro
201   1   5   10   15
202
203   Gly Leu Ile Trp Glu Asn Glu Glu Lys Ser Met Phe Arg Ile Pro Trp
204   20   25   30
205

INPUT SET: S35611.raw

```
206         Lys His Ala Gly Lys Gln Asp Tyr Asn Gln Glu Val Asp Ala Ser Ile
207             35                  40                  45
208
209         Phe Lys Ala Trp Ala Val Phe Lys Gly Lys Phe Lys Glu Gly Asp Lys
210             50                  55                  60
211
212         Ala Glu Pro Ala Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys
213         65                  70                  75                  80
214
215         Ser Pro Asp Phe Glu Glu Val Thr Asp Arg Ser Gln Leu Asp Ile Ser
216                         85                  90                  95
217
218         Glu Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
219                     100                 105
220
221   (2) INFORMATION FOR SEQ ID NO:6:
222
223         (i) SEQUENCE CHARACTERISTICS:
224               (A) LENGTH: 107 amino acids
225               (B) TYPE: amino acid
226               (C) STRANDEDNESS: single
227               (D) TOPOLOGY: linear
228
229        (ii) MOLECULE TYPE: peptide
230
231
232
233
234        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
235
236         Lys Leu Arg Asn Trp Val Val Glu Gln Val Glu Ser Gly Gln Phe Pro
237         1               5                   10                  15
238
239         Gly Val Cys Trp Asp Asp Thr Ala Lys Thr Met Phe Arg Ile Pro Trp
240                     20                  25                  30
241
242         Lys His Ala Gly Lys Gln Asp Phe Arg Glu Asp Gln Asp Ala Ala Phe
243             35                  40                  45
244
245         Phe Lys Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly Asp Thr
246             50                  55                  60
247
248         Gly Gly Pro Ala Val Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys
249         65                  70                  75                  80
250
251         Ser Ser Glu Phe Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala
252                         85                  90                  95
253
254         Glu Pro Tyr Lys Val Tyr Gln Leu Leu Pro Pro
255                     100                 105
256
257   (2) INFORMATION FOR SEQ ID NO:7:
258
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INPUT SET: S35611.raw

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

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463     (2) INFORMATION FOR SEQ ID NO:13:
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465         (i) SEQUENCE CHARACTERISTICS:
466             (A) LENGTH: 5176 base pairs
467             (B) TYPE: nucleic acid
468             (C) STRANDEDNESS: single
469             (D) TOPOLOGY: linear
470
471         (ii) MOLECULE TYPE: other nucleic acid
472
473
474         (ix) FEATURE:
475             (A) NAME/KEY: CDS
476             (B) LOCATION: 217..1569
477
478
479         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
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481     GCCTGACCAA CATGGTAAAA CCCCATCTCT GCTAAAACTA CAAAAAATTA GCTGGATGTG     60
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483     GTGGCAGGGA ACCTGTCATC CCAGCTAGTT GGGAGACTGA GGCAGGAGAA TCGCTCGATC     120
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485     TTGGGACCCA CCGCTGCCCT CAGCTCCGAG TCCAGGGCGA GTGCAGAGCA CAGCGGGCGG     180
486
487     AGGACCCCGG GCGCGGGCGC GGACGGCACG CGGGGC ATG AAC CTG GAG GGC GGC     234
488                                            Met Asn Leu Glu Gly Gly
489                                             1                   5
490
491     GGC CGA GGC GGA GAG TTC GGC ATG AGC GCG GTG AGC TGC GGC AAC GGG     282
492     Gly Arg Gly Gly Glu Phe Gly Met Ser Ala Val Ser Cys Gly Asn Gly
493             10              15                  20
494
495     AAG CTC CGC CAG TGG CTG ATC GAC CAG ATC GAC AGC GGC AAG TAC CCC     330
496     Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
497             25              30                  35
498
499     GGG CTG GTG TGG GAG AAC GAG GAG AAG AGC ATC TTC CGC ATC CCC TGG     378
500     Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Ile Phe Arg Ile Pro Trp
501         40              45                  50
502
503     AAG CAC GCG GGC AAG CAG GAC TAC AAC CGC GAG GAG GAC GCC GCG CTC     426
504     Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
505     55              60                  65                  70
506
507     TTC AAG GCT TGG GCA CTG TTT AAA GGA AAG TTC CGA GAA GGC ATC GAC     474
508     Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
509             75              80                  85
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INPUT SET: S35611.raw

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510
511    AAG CCG GAC CCT CCC ACC TGG AAG ACG CGC CTG CGG TGC GCT TTG AAC        522
512    Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
513                90              95                  100
514
515    AAG AGC AAT GAC TTT GAG GAA CTG GTT GAG CGG AGC CAG CTG GAC ATC        570
516    Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
517            105                 110                 115
518
519    TCA GAC CCG TAC AAA GTG TAC AGG ATT GTT CCT GAG GGA GCC AAA AAA        618
520    Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu Gly Ala Lys Lys
521        120                 125                 130
522
523    GGA GCC AAG CAG CTC ACC CTG GAG GAC CCG CAG ATG TCC ATG AGC CAC        666
524    Gly Ala Lys Gln Leu Thr Leu Glu Asp Pro Gln Met Ser Met Ser His
525    135                 140                 145                 150
526
527    CCC TAC ACC ATG ACA ACG CCT TAC CCT TCG CTC CCA GCC CAG CAG GTT        714
528    Pro Tyr Thr Met Thr Thr Pro Tyr Pro Ser Leu Pro Ala Gln Gln Val
529                155                 160                 165
530
531    CAC AAC TAC ATG ATG CCA CCC CTC GAC CGA AGC TGG AGG GAC TAC GTC        762
532    His Asn Tyr Met Met Pro Pro Leu Asp Arg Ser Trp Arg Asp Tyr Val
533                170                 175                 180
534
535    CCG GAT CAG CCA CAC CCG GAA ATC CCG TAC CAA TGT CCC ATG ACG TTT        810
536    Pro Asp Gln Pro His Pro Glu Ile Pro Tyr Gln Cys Pro Met Thr Phe
537            185                 190                 195
538
539    GGA CCC CGC GGC CAC CAC TGG CAA GGC CCA GCT TGT GAA AAT GGT TGC        858
540    Gly Pro Arg Gly His His Trp Gln Gly Pro Ala Cys Glu Asn Gly Cys
541        200                 205                 210
542
543    CAG GTG ACA GGA ACC TTT TAT GCT TGT GCC CCA CCT GAG TCC CAG GCT        906
544    Gln Val Thr Gly Thr Phe Tyr Ala Cys Ala Pro Pro Glu Ser Gln Ala
545    215                 220                 225                 230
546
547    CCC GGA GTC CCC ACA GAG CCA AGC ATA AGG TCT GCC GAA GCC TTG GCG        954
548    Pro Gly Val Pro Thr Glu Pro Ser Ile Arg Ser Ala Glu Ala Leu Ala
549                235                 240                 245
550
551    TTC TCA GAC TGC CGG CTG CAC ATC TGC CTG TAC TAC CGG GAA ATC CTC        1002
552    Phe Ser Asp Cys Arg Leu His Ile Cys Leu Tyr Tyr Arg Glu Ile Leu
553            250                 255                 260
554
555    GTG AAG GAG CTG ACC ACG TCC AGC CCC GAG GGC TGC CGG ATC TCC CAT        1050
556    Val Lys Glu Leu Thr Thr Ser Ser Pro Glu Gly Cys Arg Ile Ser His
557            265                 270                 275
558
559    GGA CAT ACG TAT GAC GCC AGC AAC CTG GAC CAG GTC CTG TTC CCC TAC        1098
560    Gly His Thr Tyr Asp Ala Ser Asn Leu Asp Gln Val Leu Phe Pro Tyr
561        280                 285                 290
562
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INPUT SET: S35611.raw

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563   CCA GAG GAC AAT GGC CAC AGG AAA AAC ATT GAG AAC CTG CTG AGC CAC      1146
564   Pro Glu Asp Asn Gly His Arg Lys Asn Ile Glu Asn Leu Leu Ser His
565   295             300             305             310
566
567   CTG GAG AGG GGC GTG GTC CTC TGG ATG GCC CCC GAC GGG CTC TAT GCG      1194
568   Leu Glu Arg Gly Val Val Leu Trp Met Ala Pro Asp Gly Leu Tyr Ala
569   315             320             325
570
571   AAA AGA CTG TGC CAG AGC ACG ATC TAC TGG GAC GGG CCC CTG GCG CTG      1242
572   Lys Arg Leu Cys Gln Ser Thr Ile Tyr Trp Asp Gly Pro Leu Ala Leu
573             330             335             340
574
575   TGC AAC GAC CGG CCC AAC AAA CTG GAG AGA GAC CAG ACC TGC AAG CTC      1290
576   Cys Asn Asp Arg Pro Asn Lys Leu Glu Arg Asp Gln Thr Cys Lys Leu
577             345             350             355
578
579   TTT GAC ACA CAG CAG TTC TTG TCA GAG CTG CAA GCG TTT GCT CAC CAC      1338
580   Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu Gln Ala Phe Ala His His
581       360             365             370
582
583   GGC CGC TCC CTG CCA AGA TTC CAG GTG ACT CTA TGC TTT GGA GAG GAG      1386
584   Gly Arg Ser Leu Pro Arg Phe Gln Val Thr Leu Cys Phe Gly Glu Glu
585   375             380             385             390
586
587   TTT CCA GAC CCT CAG AGG CAA AGA AAG CTC ATC ACA GCT CAC GTA GAA      1434
588   Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu Ile Thr Ala His Val Glu
589             395             400             405
590
591   CCT CTG CTA GCC AGA CAA CTA TAT TAT TTT GCT CAA CAA AAC AGT GGA      1482
592   Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe Ala Gln Gln Asn Ser Gly
593             410             415             420
594
595   CAT TTC CTG AGG GGC TAC GAT TTA CCA GAA CAC ATC AGC AAT CCA GAA      1530
596   His Phe Leu Arg Gly Tyr Asp Leu Pro Glu His Ile Ser Asn Pro Glu
597             425             430             435
598
599   GAT TAC CAC AGA TCT ATC CGC CAT TCC TCT ATT CAA GAA TGAAAAATGT      1579
600   Asp Tyr His Arg Ser Ile Arg His Ser Ser Ile Gln Glu
601       440             445             450
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603   CAAGATGAGT GGTTTTCTTT TTCCTTTTTT TTTTTTTTTT TTTTGATACG GAGATACGGG      1639
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605   GTCTTGCTCT GTCTCCCAGG CTGGAGTGCA GTGACACAAT CTCAGCTCAC TGTGACCTCC      1699
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607   GCCTCCTGGG TTCAAGAGAC TCTCCTGCCT CAGCCTCCCT GGTAGCTGGG ATTACAGGTG      1759
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609   TGAGCCACTG CACCCACCCA AGACAAGTGA TTTTCATTGT AAATATTTGA CTTTAGTGAA      1819
610
611   AGCGTCCAAT TGACTGCCCT CTTACTGTTT TGAGGAACTC AGAAGTGGAG ATTTCAGTTC      1879
612
613   AGCGGTTGAG GAGAATTGCG GCGAGACAAG CATGGAAAAT CAGTGACATC TGATTGGCAG      1939
614
615   ATGAGCTTAT TTCAAAAGGA AGGGTGGCTT TGCATTTTCT TGTGTTCTGT AGACTGCCAT      1999
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/585,023*

INPUT SET: S35611.raw

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619  TTTAATTTGT TGTAGATTAG GTCTTGCTGG AAGACAGAGA AAACTTGCCT TTCAGTATTG   2119
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621  ACACTGACTA GAGTGATGAC TGCTTGTAGG TATGTCTGTG CCATTTCTCA GGGAAGTAAG   2179
622
623  ATGTAAATTG AAGAAGCCTC ACACGTAAAA GAAATGTATT AATGTATGTA GGAGCTGCAG   2239
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625  TTCTTGTGGA AGACACTTGC TGAGTGAAGG AAATGAATCT TTGACTGAAG CCGTGCCTGT   2299
626
627  AGCCTTGGGG AGGCCCATCC CCCACCTGCC AGCGGTTTCC TGGTGTGGGT CCCTCTGCCC   2359
628
629  CACCCTCCTT CCCATTGGCT TTCTCTCCTT GGCCTTTCCT GGAAGCCAGT TAGTAAACTT   2419
630
631  CCTATTTTCT TGAGTCAAAA AACATGAGCG CTACTCTTGG ATGGGACATT TTTGTCTGTC   2479
632
633  CTACAATCTA GTAATGTCTA AGTAATGGTT AAGTTTTCTT GTTTCTGCAT CTTTTTGACC   2539
634
635  CTCATTCTTT AGAGATGCTA AAATTCTTCG CATAAAGAAG AAGAAATTAA GGAACATAAA   2599
636
637  TCTTAATACT TGAACTGTTG CCCTTCTGTC CAAGTACTTA ACTATCTGTT CCCTTCCTCT   2659
638
639  GTGCCACGCT CCTCTGTTTG TTTGGCTGTC CAGCGATCAG CCATGGCGAC ACTAAAGGAG   2719
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641  GAGGAGCCGG GGACTCCCAG GCTGGAGAGC ACTGCCAGGA CCCACCACTG GAAGCAGGAT   2779
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643  GGAGCTGACT ACGGAACTGC ACACTCAGTG GGCTGTTTCT GCTTATTTCA TCTGTTCTAT   2839
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645  GCTTCCTCGT GCCAATTATA GTTTGACAGG GCCTTAAAAT TACTTGGCTT TTTCCAAATG   2899
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647  CTTCTATTTA TAGAAATCCC AAAGACCTCC ACTTGCTTAA GTATACCTAT CACTTACATT   2959
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649  TTTGTGGTTT TGAGAAAGTA CAGCAGTAGA CTGGGGCGTC ACCTCCAGGC CGTTTCTCAT   3019
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651  ACTACAGGAT ATTTACTATT ACTCCCAGGA TTCAGCAGAA GATTGCGTTA GCTCTCAAAT   3079
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653  GTGTGTTCCT GCTTTTCTAA TGGATATTTT AAATTCATTC AACAAGCACC TAGTAAGTGC   3139
654
655  CTGCTGTATC CCTACATTAC ACAGTTCAGC CTTTATCAAG CTTAGTGAGC AGTGAGCACT   3199
656
657  GAAACATTAT TTTTTAATGT TTAAAAAGTT TCTAATATTA AAGTCAGAAT ATTAATACAA   3259
658
659  TTAATATTAA TATTAACTAC AGAAAAGACA AACAGTAGAG AACAGCAAAA AAATAAAAAG   3319
660
661  GATCTCCTTT TTTCCCAGCC CAAATTCTCC TCTCTAAAAG TGTCCACAAG AAGGGGTGTT   3379
662
663  TATTCTTCCA ACACATTTCA CTTTTCTGTA AATATACATA AACTTAAAAA GAAAACCTCA   3439
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665  TGGAGTCATC TTGCACACAC TTTTCATGCA GTGCTCTTTG TAGCTAAACA GTGAAGATTT   3499
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667  ACCTCGTTCT GCTCAGAGGC CTTGCTGTGG AGCTCCACTG CCATGTACCC AGTAGGGTTT   3559
668
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INPUT SET: S35611.raw

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669   GACATTTCAT TAGCCATGCA ACATGGATAT GTATTGGGCA GCAGACTGTG TTTCGTGAAC   3619
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671   TGCAGTGATG TATACATCTT ATAGATGCAA AGTATTTTGG GGTATATTAT CCTAAGGGAA   3679
672
673   GATAAAGATG ATATTAAGAA CTGCTGTTTC ACGGGGCCCT TACCTGTGAC CCTCTTTGCT   3739
674
675   GAAGAATATT TAACCCCACA CAGCACTTCA AAGAAGCTGT CTTGGAAGTC TGTCTCAGGA   3799
676
677   GCACCCTGTC TTCTTAATTC TCCAAGCGGA TGCTCCATTT CAATTGCTTT GTGACTTCTT   3859
678
679   CTTCTTTGTT TTTTTAAATA TTATGCTGCT TTAACAGTGG AGCTGAATTT TCTGGAAAAT   3919
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681   GCTTCTTGGC TGGGGCCACT ACCTCCTTTC CTATCTTTAC ATCTATGTGT ATGTTGACTT   3979
682
683   TTTAAAATTC TGAGTGATCC AGGGTATGAC CTAGGGAATG AACTAGCTAT GGAAATAACT   4039
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685   CAGGGTTAGG AATCCTAGCA CTTGTCTCAG GACTCTGAAA AGGAACGGCT TCCTCATTCC   4099
686
687   TTGTCTTGAT AAAGTGGAAT TGGCAAACTA GAATTTAGTT TGTACTCAGT GGACAGTGCT   4159
688
689   GTTGAAGATT TGAGGACTTG TTAAAGAGCA CTGGGTCATA TGGAAAAAAT GTATGTGTCT   4219
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691   CCCCAGGTGC ATTTTCTTGG TTTATGTCTT GTTCTTGAGA TTTTGTATAT TTAGGAAAAC   4279
692
693   CTCAAGCAGT AATTAATATC TCCTGGAACA CTATAGAGAA CCAAGTGACC GACTCATTTA   4339
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695   CAACTGAAAC CTAGGAAGCC CCTGAGTCCT GAGCGAAAAC AGGAGAGTTA GTCGCCCTAC   4399
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697   AGAAAACCCA GCTAGACTAT TGGGTATGAA CTAAAAGAG ACTGTGCCAT GGTGAGAAAA   4459
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699   ATGTAAAATC CTACAGTGGA ATGAGCAGCC CTTACAGTGT TGTTACCACC AAGGGCAGGT   4519
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701   AGGTATTAGT GTTTGAAAAA GCTGGTCTTT GAGCGAGGGC ATAAATACAG CTAGCCCCAG   4579
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703   GGGTGGAACA ACTGTGGGAG TCTTGGGTAC TCGCACCTCT TGGCTTTGTT GATGCTCCGC   4639
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705   CAGGAAGGCC ACTTGTGTGT GCGTGTCAGT TACTTTTTTA GTAACAATTC AGATCCAGTG   4699
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707   TAAACTTCCG TTCATTGCTC TCCAGTCACA TGCCCCCACT TCCCCACAGG TGAAAGTTTT   4759
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709   TCTGAAGTGT TGGGATTGGT TAAGGTCTTT ATTTGTATTA CGTATCTCCC CAAGTCCTCT   4819
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711   GTGGCCAGCT GCATCTGTCT GAATGGTGCG TGAAGGCTCT CAGACCTTAC ACACCATTTT   4879
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713   GTAAGTTATG TTTTACATGC CCCGTTTTTG AGACTGATCT CGATGCAGGT GGATCTCCTT   4939
714
715   GAGATCCTGA TAGCCTGTTA CAGGAATGAA GTAAAGGTCA GTTTTTTTTG TATTGATTTT   4999
716
717   CACAGCTTTG AGGAACATGC ATAAGAAATG TAGCTGAAGT AGAGGGGACG TGAGAGAAGG   5059
718
719   GCCAGGCCGG CAGGCCAACC CTCCTCCAAT GGAAATTCCC GTGTTGCTTC AAACTGAGAC   5119
720
721   AGATGGGACT TAACAGGCAA TGGGGTCCAC TTCCCCCTCT TCAGCATCCC CCGTACC      5176
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722
723
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822   (2)  INFORMATION FOR SEQ ID NO:15:
823
824        (i)  SEQUENCE CHARACTERISTICS:
825             (A)  LENGTH: 152 base pairs
826             (B)  TYPE: nucleic acid
827             (C)  STRANDEDNESS: single
828             (D)  TOPOLOGY: linear
829
830        (ii)  MOLECULE TYPE: DNA (genomic)
831
832
833
834
835        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:15:
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837   TTTTCTCTAC AGTCACCTCC CTGTTTACCA AAGATAATCA CAATAAGTCC AGTTTACTTA    60
838
839   CAAAACAAGT TTAGTTATTA GAGGAAACTA AAACTTCAGG ATTCAGTCCA GATAATTTTT    120
840
841   AAAAACTCTA AAACAATGGA CAGGGCTAGA AT                                  152
842
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843   (2)  INFORMATION FOR SEQ ID NO:16:
844
845        (i)  SEQUENCE CHARACTERISTICS:
846             (A)  LENGTH: 152 base pairs
847             (B)  TYPE: nucleic acid
848             (C)  STRANDEDNESS: single
849             (D)  TOPOLOGY: linear
850
851        (ii)  MOLECULE TYPE: other nucleic acid
852
853
854
855
856        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:16:
857
858   TGGGCTCGGC CTGGTGGGGC AGCCACAGCG GGACGCAGTA GTGAAAGTCC AGTTTACTTA    60
859
860   CAAAACAAGT TTAGTTATTA GAGGAAACTA AAACTTCAGG ATTCAGCAGG GCATGAGGAG    120
861
862   GCAGCTCCTC ACCCTCCCTT TCTCTTTTGT AC                                  152
863
```

```
864   (2)  INFORMATION FOR SEQ ID NO:17:
865
866        (i)  SEQUENCE CHARACTERISTICS:
867             (A)  LENGTH: 152 base pairs
868             (B)  TYPE: nucleic acid
869             (C)  STRANDEDNESS: single
```

```
870              (D) TOPOLOGY: linear
871
872         (ii) MOLECULE TYPE: DNA (genomic)
873
874
875
876
877         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
878
879    TGGGCTCGGC CTTGGTGGGG CAGCCACAGC GGGACGCAAG TAGTGAGGGC ACTCAGAACG        60
880
881    CCACTCAGCC CCGACAGGGC ACTCAGAACG CCACTCAGCC CCGACAGGCA GGGCACGAGG       120
882
883    AGGCAGCTCC TCACCCTCCC TTTCTCTTTT GT                                     152
884
```